

0590
0502



#2

OIPE

RAW SEQUENCE LISTING DATE: 05/07/2002
PATENT APPLICATION: US/10/086,208 TIME: 11:26:07

Input Set : N:\CrF3\RULE60\10086208.raw
Output Set: N:\CRF3\05072002\J086208.raw

SEQUENCE LISTING

ENTERED

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PATENT APPLICATION: US/10/086,208

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64	1	5	10	15	
66	Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe				
67	20	25	30		
69	His Cys Gln Val Cys Phe Thr Thr Lys Gly Leu Gly Ile Ser Tyr Gly				
70	35	40	45		
72	Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr				
73	50	55	60		
75	His Gln Val Ser Leu Ser Lys Gln				
76	65	70			
78	(2) INFORMATION FOR SEQ ID NO: 2:				
80	(i) SEQUENCE CHARACTERISTICS:				
81	(A) LENGTH: 912 base pairs				
82	(B) TYPE: nucleic acid				
83	(C) STRANDEDNESS: double				
84	(D) TOPOLOGY: linear				
86	(ii) MOLECULE TYPE: cDNA				
89	(ix) FEATURE:				
90	(A) NAME/KEY: CDS				
91	(B) LOCATION: join(1..876, 883..912)				
94	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:				
96	GAG CTC TAC AAA TCC GGG GAT CCG GGT GAA GAT CCG CGT TTA GAG CCG			48	
97	Glu Leu Tyr Lys Ser Gly Asp Pro Gly Glu Asp Pro Arg Leu Glu Pro				
98	1 5 10 15				
100	TGG AAA CAC CCG GGT TCT GGT TCT GTC GAC CCT AAC CTT GAA CCT TGG			96	
101	Trp Lys His Pro Gly Ser Gly Ser Val Asp Pro Asn Leu Glu Pro Trp				
102	20 25 30				
104	AAG CAT CCT GGC AGC TCC GGA GTC GAT CCC AAA CTC GAG CCC TGG AAA			144	
105	Lys His Pro Gly Ser Ser Gly Val Asp Pro Lys Leu Glu Pro Trp Lys				
106	35 40 45				
108	CAC CCC GGA AGT TCG GGG GTA GAC CCA TCT CTG GAA CCA TGG AAG CAT			192	
109	His Pro Gly Ser Ser Gly Val Asp Pro Ser Leu Glu Pro Trp Lys His				
110	50 55 60				
112	CCA GGG AGT GGT AGC GTG AAT CCG TCA TTA GAG CCG TGG AAA CAC CCG			240	
113	Pro Gly Ser Gly Ser Val Asn Pro Ser Leu Glu Pro Trp Lys His Pro				
114	65 70 75 80				
116	GGT TCA TCT GGA GTT GAT CCT CGC TTG GAA CCT TGG GAG CAT CCT GGT			288	
117	Gly Ser Ser Gly Val Asp Pro Arg Leu Glu Pro Trp Glu His Pro Gly				
118	85 90 95				
120	TCG TCC GGT GTA GAC CCC CGA CTT GAG CCC TGG AAT CAC CTC GGG AGT			336	
121	Ser Ser Gly Val Asp Pro Arg Leu Glu Pro Trp Asn His Leu Gly Ser				
122	100 105 110				
124	TCA GGC GTA GAT CAT CGG CTC GAA CCA TGG AAA CAT CCA GGT TCT GGA			384	
125	Ser Gly Val Asp His Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gly				
126	115 120 125				
128	GAT CTG CGC CAG CGG CGA CGT ACT CCT CAG GAT TCT GGA TCT CGA CAA			432	
129	Asp Leu Arg Gln Arg Arg Arg Thr Pro Gln Asp Ser Gly Ser Arg Gln				
130	130 135 140				
132	CGT CGG CGC CCT CCC CAA GAC TCC TCA GGA CGG CAG CGC CGA CGA CCC			480	
133	Arg Arg Arg Pro Pro Gln Asp Ser Ser Gly Arg Gln Arg Arg Arg Pro				

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134	145	150	155	160	
136	CCA CAG GGT TCA GGT TCA CGT CAA CGA CGC GGT CCA CCC CAA GGC TCG				528
137	Pro Gln Gly Ser Gly Ser Arg Gln Arg Arg Gly Pro Pro Gln Gly Ser				
138	165	170	175		
140	GGT TCG CGC CAG CGG CGA CGT CCG CCT CAG AAC TCT AGT GGA CGA CAA				576
141	Gly Ser Arg Gln Arg Arg Pro Pro Gln Asn Ser Ser Gly Arg Gln				
142	180	185	190		
144	CGT CGG CGC TCT CCC CAA GAT TCC GGC GGG CGG CAG CGC CGT CGA TCA				624
145	Arg Arg Arg Ser Pro Gln Asp Ser Gly Gly Arg Gln Arg Arg Arg Ser				
146	195	200	205		
148	CCA CAG AAC TCA GGT GGG CGT CAA CGA CGC CGG ACT CCG CAA TCT TCA				672
149	Pro Gln Asn Ser Gly Gly Arg Gln Arg Arg Arg Thr Pro Gln Ser Ser				
150	210	215	220		
152	TCC GGC CGC CAG CGG CGA CGT GCC CAT CAG AAT AGC GGC AGC CGA CAA				720
153	Ser Gly Arg Gln Arg Arg Ala His Gln Asn Ser Gly Ser Arg Gln				
154	225	230	235	240	
156	CGT CGG CGC GCA CAC CAA GAC AGC AGT GGG CGG CAG CGC CGT CGA GCG				768
157	Arg Arg Arg Ala His Gln Asp Ser Ser Gly Arg Gln Arg Arg Arg Ala				
158	245	250	255		
160	CCT GAA GAT AGT GGT TCT CGT CAA CGA CGC CGG GCT CCC CCT GAC AGC				816
161	Pro Glu Asp Ser Gly Ser Arg Gln Arg Arg Arg Ala Pro Pro Asp Ser				
162	260	265	270		
164	TCC GGA CGC CAG CGG CAA CGT GCA CCA GAT AGT TCC TCA GGT CAT CAC				864
165	Ser Gly Arg Gln Arg Ala Pro Asp Ser Ser Gly His His				
166	275	280	285		
168	CAC CAT CAT CAC TAATAA GAA TTC GGA TCC TCT AGA GTC GAC AAG CTT				912
169	His His His Glu Phe Gly Ser Ser Arg Val Asp Lys Leu				
170	290	295	300		

173 (2) INFORMATION FOR SEQ ID NO: 3:

175 (i) SEQUENCE CHARACTERISTICS:

176 (A) LENGTH: 302 amino acids

177 (B) TYPE: amino acid

178 (D) TOPOLOGY: linear

180 (ii) MOLECULE TYPE: protein

182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

184	Glu Leu Tyr Lys Ser Gly Asp Pro Gly Glu Asp Pro Arg Leu Glu Pro			
185	1	5	10	15
187	Trp Lys His Pro Gly Ser Gly Ser Val Asp Pro Asn Leu Glu Pro Trp			
188	20	25	30	
190	Lys His Pro Gly Ser Ser Gly Val Asp Pro Lys Leu Glu Pro Trp Lys			
191	35	40	45	
193	His Pro Gly Ser Ser Gly Val Asp Pro Ser Leu Glu Pro Trp Lys His			
194	50	55	60	
196	Pro Gly Ser Gly Ser Val Asn Pro Ser Leu Glu Pro Trp Lys His Pro			
197	65	70	75	80
199	Gly Ser Ser Gly Val Asp Pro Arg Leu Glu Pro Trp Glu His Pro Gly			
200	85	90	95	
202	Ser Ser Gly Val Asp Pro Arg Leu Glu Pro Trp Asn His Leu Gly Ser			
203	100	105	110	

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205 Ser Gly Val Asp His Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gly
206 115 120 125
208 Asp Leu Arg Gln Arg Arg Arg Thr Pro Gln Asp Ser Gly Ser Arg Gln
209 130 135 140
211 Arg Arg Arg Pro Pro Gln Asp Ser Ser Gly Arg Gln Arg Arg Arg Pro
212 145 150 155 160
214 Pro Gln Gly Ser Gly Ser Arg Gln Arg Arg Gly Pro Pro Gln Gly Ser
215 165 170 175
217 Gly Ser Arg Gln Arg Arg Arg Pro Pro Gln Asn Ser Ser Gly Arg Gln
218 180 185 190
220 Arg Arg Arg Ser Pro Gln Asp Ser Gly Gly Arg Gln Arg Arg Arg Ser
221 195 200 205
223 Pro Gln Asn Ser Gly Gly Arg Gln Arg Arg Arg Thr Pro Gln Ser Ser
224 210 215 220
226 Ser Gly Arg Gln Arg Arg Arg Ala His Gln Asn Ser Gly Ser Arg Gln
227 225 230 235 240
229 Arg Arg Arg Ala His Gln Asp Ser Ser Gly Arg Gln Arg Arg Arg Ala
230 245 250 255
232 Pro Glu Asp Ser Gly Ser Arg Gln Arg Arg Arg Ala Pro Pro Asp Ser
233 260 265 270
235 Ser Gly Arg Gln Arg Gln Arg Ala Pro Asp Ser Ser Ser Gly His His
236 275 280 285
238 His His His Glu Phe Gly Ser Ser Arg Val Asp Lys Leu
239 290 295 300

241 (2) INFORMATION FOR SEQ ID NO: 4:

243 (i) SEQUENCE CHARACTERISTICS:
244 (A) LENGTH: 9 amino acids
245 (B) TYPE: amino acid
246 (C) STRANDEDNESS:
247 (D) TOPOLOGY: linear

249 (ii) MOLECULE TYPE: peptide

254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

256 Arg Lys Lys Arg Arg Gln Arg Arg Arg
257 1 5

259 (2) INFORMATION FOR SEQ ID NO: 5:

261 (i) SEQUENCE CHARACTERISTICS:
262 (A) LENGTH: 6 amino acids
263 (B) TYPE: amino acid
264 (C) STRANDEDNESS:
265 (D) TOPOLOGY: linear

267 (ii) MOLECULE TYPE: peptide

272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

274 Gly Arg Gly Asp Ser Pro
275 1 5

277 (2) INFORMATION FOR SEQ ID NO: 6:

279 (i) SEQUENCE CHARACTERISTICS:
280 (A) LENGTH: 7 amino acids
281 (B) TYPE: amino acid
282 (C) STRANDEDNESS:

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283 (D) TOPOLOGY: linear
285 (ii) MOLECULE TYPE: peptide
290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
292 Val Asp Pro Arg Leu Glu Pro
293 1 5
295 (2) INFORMATION FOR SEQ ID NO: 7:
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 7 amino acids
299 (B) TYPE: amino acid
300 (C) STRANDEDNESS:
301 (D) TOPOLOGY: linear
303 (ii) MOLECULE TYPE: peptide
308 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
310 Val Asp Pro Lys Leu Glu Pro
311 1 5
313 (2) INFORMATION FOR SEQ ID NO: 8:
315 (i) SEQUENCE CHARACTERISTICS:
316 (A) LENGTH: 7 amino acids
317 (B) TYPE: amino acid
318 (C) STRANDEDNESS:
319 (D) TOPOLOGY: linear
321 (ii) MOLECULE TYPE: peptide
326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
328 Val Asp Pro Ser Leu Glu Pro
329 1 5
331 (2) INFORMATION FOR SEQ ID NO: 9:
333 (i) SEQUENCE CHARACTERISTICS:
334 (A) LENGTH: 7 amino acids
335 (B) TYPE: amino acid
336 (C) STRANDEDNESS:
337 (D) TOPOLOGY: linear
339 (ii) MOLECULE TYPE: peptide
344 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
346 Val Asp Pro Asn Leu Glu Pro
347 1 5
349 (2) INFORMATION FOR SEQ ID NO: 10:
351 (i) SEQUENCE CHARACTERISTICS:
352 (A) LENGTH: 6 amino acids
353 (B) TYPE: amino acid
354 (C) STRANDEDNESS:
355 (D) TOPOLOGY: linear
357 (ii) MOLECULE TYPE: peptide
360 (ix) FEATURE:
361 (A) NAME/KEY: Binding-site
362 (B) LOCATION: 6
363 (D) OTHER INFORMATION: /note= "an amide is attached to the
364 Ser in position 6"
367 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
369 Trp Lys His Pro Gly Ser

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/07/2002
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Input Set : N:\Crf3\RULE60\10086208.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:36; Xaa Pos.1,5,9
Seq#:37; Xaa Pos.1,3,13
Seq#:38; Xaa Pos.1,4,5,6,7
Seq#:39; Xaa Pos.1,4,7,14
Seq#:58; Xaa Pos.4
Seq#:86; Xaa Pos.4
Seq#:87; Xaa Pos.2
Seq#:88; Xaa Pos.3,4,5,6
Seq#:89; Xaa Pos.3,6
Seq#:110; Xaa Pos.3,6
Seq#:124; Xaa Pos.6

VERIFICATION SUMMARY DATE: 05/07/2002
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Input Set : N:\Crf3\RULE60\10086208.raw
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:1951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
L:1992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88 after pos.:0
L:2021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:0
L:2453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110 after pos.:0
L:2720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:0